

**Table S1:** qPCR primers used for quantification and temperature profiles

Target gene	Primer	Fragment size [bp]	Reference	Primer sequence	Thermal profile	No of cycles
Bacterial 16S rRNA	341F	194	Muyzer et al., 1993	CCTACGGGAGGCAGCAG	95°C-15s/60°C-30s/72°C-30s /80°C-15s	35
	534			ATTACCGCGCTGCTGGCA		
Crenarchaeal 16S rRNA	Crenar771F	229	Ochsenreiter et al., 2003	ACGGTGAGGGATGAAAGCT	95°C-15s/55°C-30s/72°C-30s /80°C-15s	35
	Crenar975R			CGGCCTTGACTCCAATTG		
Fungal ITS	ITS 3F	336	White et al., 1990	GCATCGATGAAGAACGCAGC	95°C-15s/55°C-30s/72°C-30s /80°C-15s	35
	ITS 4R			TCCTCCGCTTATTGATATGC		
Bacterial ammonium monooxygenase:	AmoA1F	491	Leininger et al. 2006	GGGGTTCTACTGGTGGT	95°C-15s/55°C-30s/72°C-30s /80°C-15s	35
<i>amoA</i>	AmoA2R			CCCCTCKGSAAAGCCTCTTC		
Archaeal ammonium monooxygenase:	crenamoA23F	628	Tourna et al., 2008	ATGGTCTGGCTWAGACG	95°C-15s/55°C-30s/72°C-30s /80°C-15s	35
<i>amoA</i>	crenamoA616R			GCCATCCATCTGTATGTCCA		
Cu-containing nitrite reductase:	nirK 876F	164	Henry et al., 2004	ATYGGCGGVCAYGCGA	95°C-15s/63-58°C-30s/72°C-30s /80°C-15s	6
<i>nirK</i>	nirK 1040R			GCCTCGATCAGRRTRTGGTT	95°C-15s/58°C-30s/72°C-30s /80°C-15s	35
Nitrite reductase:	nirS4QF	410	Throbäck et al., 2004	GTSAACCGYSAAGGARACSGG	95°C-15s/63-58°C-30s/72°C-30s /80°C-15s	6
<i>nirS</i>	nirS6QR			GASTTCGGRTGSGTCTTSAYGAA	95°C-15s/58°C-30s/72°C-30s /80°C-15s	35
Nitrous oxide reductase:	nosZ 1840F	267	Henry et al., 2006	CGCRACGGCAASAAGGTSMSSGT	95°C-15s/54°C-30s/72°C-30s /80°C-15s	35
<i>nosZ (cladeI)</i>	nosZ 2090R			CAKRTGCAKSGCRTGGCAGAA		
Nitrous oxide reductase:	1153 nosZ 8F	698	Jones et al., 2013	CTIGGICCIYTKCAYAC	95°C-15s/54°C-30s/72°C-30s /80°C-15s	35
<i>nosZ (cladeII)</i>	1888 nosZ 29R			GCIGAICARAATCBGTRC		

**Table S2:** p-values for the main effects of the different treatments, sampling time and depth, and their interactions for quantitative real time PCR gene copy estimation (bacterial and Crenarchaeal 16S rRNA, fungal ITS, archaeal (AOA) and bacterial *amoA* (AOB), *nirK* and *nirS*, *nosZI* and *nosZII*) as determined by three-way ANOVA

Source of variation	Bacterial 16S rRNA	Crenarchaeal 16S rRNA	Fungal ITS	<i>amoA</i> AOA	<i>amoA</i> AOB	<i>nirK</i>	<i>nirS</i>	<i>nosZI</i>	<i>nosZII</i>
Treatment	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.0003	<0.0001	<0.0001	<0.0001
Sampling	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<.0001	<0.0001	<0.0001	<0.0001
Depth	<0.0001	0.2965	<0.0001	0.0004	<0.0001	0.0001	<0.0001	<0.0001	<0.0001
Treatment:Sampling	<0.0001	<0.0001	0.0012	0.0001	<0.0001	0.0904	<0.0001	0.0010	<0.0001
Treatment:Depth	<0.0001	0.8653	<0.0001	0.1296	<0.0001	0.0343	<0.0001	<0.0001	<0.0001
Sampling:Depth	0.0726	0.1375	0.4755	0.0033	<0.0001	0.0943	0.0016	0.2412	0.4379
Treatment:Sampling:Depth	0.0020	0.4935	<0.0001	0.2826	<0.0001	0.0448	0.0055	0.1396	0.0744

**Table S3:** Bacterial, Crenarchaeal 16S rRNA and fungal ITS copy numbers in CON (control), INC (straw incorporated in 0 – 10 cm soil layer) and SRF (straw applied at the soil surface) soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

Treatment	Depth (cm)	16S rRNA bacteria			16S rRNA Crenarchaea			ITS fungi		
		1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point	1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point	1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point
SRF	0-1	1.83×10 <sup>9</sup> ±1.39×10 <sup>8</sup>	1.51×10 <sup>9</sup> ±1.47×10 <sup>7</sup>	2.55×10 <sup>9</sup> ±2.91×10 <sup>8</sup>	8.33×10 <sup>7</sup> ±6.39×10 <sup>6</sup>	7.56×10 <sup>7</sup> ±1.09×10 <sup>7</sup>	1.17×10 <sup>8</sup> ±1.06×10	1.60×10 <sup>8</sup> ±1.95×10	1.37×10 <sup>8</sup> ±1.62×10	3.27×10 <sup>8</sup> ±5.32×10
INC		1.79×10 <sup>9</sup> ±1.49×10 <sup>8</sup>	1.57×10 <sup>9</sup> ±2.07×10 <sup>8</sup>	2.47×10 <sup>9</sup> ±1.23×10 <sup>8</sup>	9.17×10 <sup>7</sup> ±2.73×10 <sup>6</sup>	6.56×10 <sup>7</sup> ±8.77×10 <sup>6</sup>	1.02×10 <sup>8</sup> ±9.84×10	1.58×10 <sup>8</sup> ±2.83×10	1.25×10 <sup>8</sup> ±2.18×10	1.69×10 <sup>8</sup> ±7.03×10
CON		1.80×10 <sup>9</sup> ±1.69×10 <sup>8</sup>	1.16×10 <sup>9</sup> ±9.28×10 <sup>7</sup>	1.99×10 <sup>9</sup> ±2.95×10 <sup>8</sup>	8.17×10 <sup>7</sup> ±7.94×10 <sup>6</sup>	5.80×10 <sup>7</sup> ±7.51×10 <sup>6</sup>	9.15×10 <sup>7</sup> ±1.07×10	8.47×10 <sup>7</sup> ±2.32×10	5.21×10 <sup>7</sup> ±6.51×10	1.65×10 <sup>8</sup> ±5.00×10
SRF+S		3.08×10 <sup>9</sup> ±1.69×10 <sup>8</sup>	2.75×10 <sup>9</sup> ±2.32×10 <sup>8</sup>	3.52×10 <sup>9</sup> ±3.17×10 <sup>8</sup>	7.08×10 <sup>7</sup> ±7.51×10 <sup>6</sup>	8.25×10 <sup>7</sup> ±5.88×10 <sup>6</sup>	9.82×10 <sup>7</sup> ±6.55×10	2.24×10 <sup>8</sup> ±2.49×10	1.87×10 <sup>8</sup> ±1.35×10	3.56×10 <sup>8</sup> ±7.72×10
INS+S		3.56×10 <sup>9</sup> ±5.16×10 <sup>8</sup>	4.10×10 <sup>9</sup> ±5.64×10 <sup>8</sup>	3.81×10 <sup>9</sup> ±1.48×10 <sup>8</sup>	5.84×10 <sup>7</sup> ±1.03×10 <sup>7</sup>	1.22×10 <sup>8</sup> ±1.33×10 <sup>7</sup>	1.15×10 <sup>8</sup> ±4.50×10	2.68×10 <sup>8</sup> ±6.21×10	4.60×10 <sup>8</sup> ±4.72×10	2.06×10 <sup>8</sup> ±1.43×10
CON+S		4.64×10 <sup>9</sup> ±5.82×10 <sup>8</sup>	7.03×10 <sup>9</sup> ±7.71×10 <sup>8</sup>	4.97×10 <sup>9</sup> ±4.47×10 <sup>8</sup>	7.55×10 <sup>7</sup> ±5.81×10 <sup>6</sup>	1.22×10 <sup>8</sup> ±1.13×10 <sup>7</sup>	1.35×10 <sup>8</sup> ±1.79×10	1.12×10 <sup>8</sup> ±1.33×10	1.95×10 <sup>8</sup> ±2.23×10	3.29×10 <sup>8</sup> ±4.99×10
SRF	1-10	1.33×10 <sup>9</sup> ±5.72×10 <sup>7</sup>	1.45×10 <sup>9</sup> ±1.85×10 <sup>8</sup>	1.87×10 <sup>9</sup> ±9.43×10 <sup>7</sup>	8.20×10 <sup>7</sup> ±3.22×10 <sup>6</sup>	1.02×10 <sup>8</sup> ±1.55×10 <sup>7</sup>	1.23×10 <sup>8</sup> ±3.64×10	8.79×10 <sup>7</sup> ±1.38×10	7.00×10 <sup>7</sup> ±1.63×10	1.21×10 <sup>8</sup> ±7.96×10
INC		1.48×10 <sup>9</sup> ±1.41×10 <sup>8</sup>	9.41×10 <sup>8</sup> ±6.13×10 <sup>7</sup>	2.13×10 <sup>9</sup> ±2.61×10 <sup>8</sup>	9.36×10 <sup>7</sup> ±5.20×10 <sup>6</sup>	6.53×10 <sup>7</sup> ±5.80×10 <sup>6</sup>	1.14×10 <sup>8</sup> ±5.20×10	1.50×10 <sup>8</sup> ±1.19×10	1.53×10 <sup>8</sup> ±2.50×10	2.26×10 <sup>8</sup> ±2.37×10
CON		1.60×10 <sup>9</sup> ±6.12×10 <sup>7</sup>	8.83×10 <sup>8</sup> ±2.18×10 <sup>7</sup>	1.69×10 <sup>9</sup> ±1.62×10 <sup>8</sup>	8.41×10 <sup>7</sup> ±4.42×10 <sup>6</sup>	6.31×10 <sup>7</sup> ±3.24×10 <sup>6</sup>	1.02×10 <sup>8</sup> ±5.72×10	5.45×10 <sup>7</sup> ±3.02×10	3.96×10 <sup>7</sup> ±3.37×10	9.44×10 <sup>7</sup> ±1.01×10
SRF+S		1.19×10 <sup>9</sup> ±5.87×10 <sup>7</sup>	1.59×10 <sup>9</sup> ±1.97×10 <sup>8</sup>	2.09×10 <sup>9</sup> ±1.74×10 <sup>8</sup>	7.98×10 <sup>7</sup> ±3.06×10 <sup>6</sup>	8.13×10 <sup>7</sup> ±7.65×10 <sup>6</sup>	1.10×10 <sup>8</sup> ±1.14×10	8.62×10 <sup>7</sup> ±8.75×10	7.04×10 <sup>7</sup> ±1.50×10	9.64×10 <sup>7</sup> ±1.70×10
INS+S		1.51×10 <sup>9</sup> ±1.50×10 <sup>8</sup>	1.89×10 <sup>9</sup> ±2.06×10 <sup>8</sup>	2.46×10 <sup>9</sup> ±8.29×10 <sup>7</sup>	8.23×10 <sup>7</sup> ±4.83×10 <sup>6</sup>	9.98×10 <sup>7</sup> ±7.26×10 <sup>6</sup>	1.17×10 <sup>8</sup> ±1.05×10	2.08×10 <sup>8</sup> ±1.05×10	2.39×10 <sup>8</sup> ±2.52×10	3.60×10 <sup>8</sup> ±5.65×10
CON+S		1.37×10 <sup>9</sup> ±4.66×10 <sup>7</sup>	1.93×10 <sup>9</sup> ±9.97×10 <sup>7</sup>	2.36×10 <sup>9</sup> ±2.97×10 <sup>8</sup>	8.09×10 <sup>7</sup> ±6.57×10 <sup>6</sup>	1.05×10 <sup>8</sup> ±9.01×10 <sup>6</sup>	1.37×10 <sup>8</sup> ±7.42×10	5.36×10 <sup>7</sup> ±4.80×10	8.26×10 <sup>7</sup> ±1.41×10	1.47×10 <sup>8</sup> ±2.12×10
SRF	10-20	1.52×10 <sup>9</sup> ±7.21×10 <sup>7</sup>	1.68×10 <sup>9</sup> ±2.41×10 <sup>8</sup>	2.01×10 <sup>9</sup> ±1.36×10 <sup>8</sup>	7.59×10 <sup>7</sup> ±2.87×10 <sup>6</sup>	9.62×10 <sup>7</sup> ±9.40×10 <sup>6</sup>	1.31×10 <sup>8</sup> ±5.71×10	5.37×10 <sup>7</sup> ±1.43×10	7.37×10 <sup>7</sup> ±1.19×10	1.43×10 <sup>8</sup> ±4.83×10
INC		1.85×10 <sup>9</sup> ±1.23×10 <sup>8</sup>	1.53×10 <sup>9</sup> ±1.83×10 <sup>8</sup>	2.36×10 <sup>9</sup> ±8.27×10 <sup>7</sup>	8.75×10 <sup>7</sup> ±7.74×10 <sup>6</sup>	4.97×10 <sup>7</sup> ±3.21×10 <sup>6</sup>	1.27×10 <sup>8</sup> ±1.53×10	6.83×10 <sup>7</sup> ±8.61×10	4.39×10 <sup>7</sup> ±4.45×10	1.21×10 <sup>8</sup> ±2.33×10
CON		1.53×10 <sup>9</sup> ±3.79×10 <sup>7</sup>	1.03×10 <sup>9</sup> ±2.57×10 <sup>7</sup>	1.93×10 <sup>9</sup> ±1.17×10 <sup>8</sup>	8.90×10 <sup>7</sup> ±5.06×10 <sup>6</sup>	5.79×10 <sup>7</sup> ±2.61×10 <sup>6</sup>	1.10×10 <sup>8</sup> ±1.13×10	6.41×10 <sup>7</sup> ±7.92×10	3.87×10 <sup>7</sup> ±4.48×10	1.09×10 <sup>8</sup> ±2.00×10
SRF+S		1.66×10 <sup>9</sup> ±4.84×10 <sup>7</sup>	1.79×10 <sup>9</sup> ±9.97×10 <sup>7</sup>	2.36×10 <sup>9</sup> ±2.14×10 <sup>8</sup>	7.07×10 <sup>7</sup> ±2.52×10 <sup>6</sup>	8.12×10 <sup>7</sup> ±7.94×10 <sup>6</sup>	1.06×10 <sup>8</sup> ±6.49×10	4.74×10 <sup>7</sup> ±2.12×10	5.77×10 <sup>7</sup> ±3.27×10	7.48×10 <sup>7</sup> ±9.50×10
INS+S		1.94×10 <sup>9</sup> ±1.48×10 <sup>8</sup>	2.60×10 <sup>9</sup> ±5.40×10 <sup>7</sup>	3.24×10 <sup>9</sup> ±2.13×10 <sup>8</sup>	7.71×10 <sup>7</sup> ±8.23×10 <sup>6</sup>	1.03×10 <sup>8</sup> ±6.86×10 <sup>6</sup>	1.18×10 <sup>8</sup> ±2.29×10	7.96×10 <sup>7</sup> ±1.58×10	1.44×10 <sup>8</sup> ±3.92×10	1.09×10 <sup>8</sup> ±1.06×10
CON+S		1.37×10 <sup>9</sup> ±1.20×10 <sup>8</sup>	2.16×10 <sup>9</sup> ±2.23×10 <sup>8</sup>	2.76×10 <sup>9</sup> ±3.01×10 <sup>8</sup>	7.34×10 <sup>7</sup> ±2.64×10 <sup>6</sup>	1.03×10 <sup>8</sup> ±2.12×10 <sup>6</sup>	1.33×10 <sup>8</sup> ±1.90×10	6.63×10 <sup>7</sup> ±4.40×10	9.88×10 <sup>7</sup> ±2.68×10	1.84×10 <sup>8</sup> ±7.45×10

**Table S4:** Crenarchaeal (AOA) and bacterial (AOB) *amoA* gene abundances in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

Treatment	Depth (cm)	amoA AOA						amoA AOB					
		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point	
SRF	0-1	1.18×10 <sup>7</sup>	±	1.02×10 <sup>6</sup>	9.26×10 <sup>6</sup>	±	1.30×10 <sup>6</sup>	1.87×10 <sup>7</sup>	±	1.05×10 <sup>6</sup>	1.06×10 <sup>6</sup>	±	7.91×10 <sup>4</sup>
INC		1.53×10 <sup>7</sup>	±	1.02×10 <sup>6</sup>	1.02×10 <sup>7</sup>	±	1.19×10 <sup>6</sup>	2.06×10 <sup>7</sup>	±	1.13×10 <sup>6</sup>	1.28×10 <sup>6</sup>	±	7.77×10 <sup>4</sup>
CON		1.29×10 <sup>7</sup>	±	1.51×10 <sup>6</sup>	8.23×10 <sup>6</sup>	±	1.39×10 <sup>6</sup>	1.65×10 <sup>7</sup>	±	2.04×10 <sup>6</sup>	1.42×10 <sup>6</sup>	±	1.07×10 <sup>5</sup>
SRF+S		9.11×10 <sup>6</sup>	±	4.12×10 <sup>5</sup>	1.43×10 <sup>7</sup>	±	1.71×10 <sup>6</sup>	2.44×10 <sup>7</sup>	±	2.16×10 <sup>6</sup>	2.20×10 <sup>6</sup>	±	4.99×10 <sup>5</sup>
INS+S		9.35×10 <sup>6</sup>	±	1.92×10 <sup>6</sup>	2.24×10 <sup>7</sup>	±	2.69×10 <sup>6</sup>	3.08×10 <sup>7</sup>	±	2.06×10 <sup>6</sup>	2.37×10 <sup>6</sup>	±	5.12×10 <sup>5</sup>
CON+S		1.26×10 <sup>7</sup>	±	1.38×10 <sup>6</sup>	1.96×10 <sup>7</sup>	±	2.95×10 <sup>6</sup>	2.89×10 <sup>7</sup>	±	4.56×10 <sup>6</sup>	2.71×10 <sup>6</sup>	±	3.95×10 <sup>5</sup>
SRF	1-10	1.40×10 <sup>7</sup>	±	3.66×10 <sup>5</sup>	1.76×10 <sup>7</sup>	±	2.52×10 <sup>6</sup>	2.63×10 <sup>7</sup>	±	1.65×10 <sup>6</sup>	9.14×10 <sup>5</sup>	±	4.37×10 <sup>4</sup>
INC		1.42×10 <sup>7</sup>	±	7.06×10 <sup>5</sup>	1.06×10 <sup>7</sup>	±	1.43×10 <sup>6</sup>	2.10×10 <sup>7</sup>	±	1.09×10 <sup>6</sup>	1.10×10 <sup>6</sup>	±	1.31×10 <sup>5</sup>
CON		1.31×10 <sup>7</sup>	±	8.33×10 <sup>5</sup>	9.96×10 <sup>6</sup>	±	7.84×10 <sup>5</sup>	2.06×10 <sup>7</sup>	±	1.51×10 <sup>6</sup>	1.10×10 <sup>6</sup>	±	1.18×10 <sup>5</sup>
SRF+S		1.08×10 <sup>7</sup>	±	6.30×10 <sup>5</sup>	1.30×10 <sup>7</sup>	±	6.29×10 <sup>5</sup>	2.77×10 <sup>7</sup>	±	5.25×10 <sup>6</sup>	1.03×10 <sup>6</sup>	±	2.90×10 <sup>4</sup>
INS+S		1.29×10 <sup>7</sup>	±	9.42×10 <sup>5</sup>	1.85×10 <sup>7</sup>	±	7.99×10 <sup>5</sup>	3.22×10 <sup>7</sup>	±	2.76×10 <sup>6</sup>	1.78×10 <sup>6</sup>	±	2.85×10 <sup>5</sup>
CON+S		1.26×10 <sup>7</sup>	±	1.77×10 <sup>6</sup>	1.96×10 <sup>7</sup>	±	1.77×10 <sup>6</sup>	3.70×10 <sup>7</sup>	±	4.69×10 <sup>6</sup>	9.85×10 <sup>5</sup>	±	1.38×10 <sup>5</sup>
SRF	10-20	1.29×10 <sup>7</sup>	±	1.36×10 <sup>6</sup>	1.72×10 <sup>7</sup>	±	1.69×10 <sup>6</sup>	2.73×10 <sup>7</sup>	±	1.18×10 <sup>6</sup>	8.05×10 <sup>5</sup>	±	1.14×10 <sup>5</sup>
INC		1.31×10 <sup>7</sup>	±	1.82×10 <sup>6</sup>	8.42×10 <sup>6</sup>	±	7.15×10 <sup>5</sup>	2.94×10 <sup>7</sup>	±	1.83×10 <sup>6</sup>	8.74×10 <sup>5</sup>	±	1.70×10 <sup>5</sup>
CON		1.53×10 <sup>7</sup>	±	8.76×10 <sup>5</sup>	9.64×10 <sup>6</sup>	±	5.73×10 <sup>5</sup>	2.27×10 <sup>7</sup>	±	2.60×10 <sup>6</sup>	1.03×10 <sup>6</sup>	±	4.07×10 <sup>4</sup>
SRF+S		9.74×10 <sup>6</sup>	±	3.26×10 <sup>5</sup>	1.38×10 <sup>7</sup>	±	1.62×10 <sup>6</sup>	2.68×10 <sup>7</sup>	±	2.73×10 <sup>6</sup>	6.41×10 <sup>5</sup>	±	6.52×10 <sup>4</sup>
INS+S		1.18×10 <sup>7</sup>	±	1.31×10 <sup>6</sup>	1.86×10 <sup>7</sup>	±	2.51×10 <sup>6</sup>	3.14×10 <sup>7</sup>	±	1.54×10 <sup>6</sup>	1.06×10 <sup>6</sup>	±	1.59×10 <sup>5</sup>
CON+S		1.36×10 <sup>7</sup>	±	8.47×10 <sup>5</sup>	1.85×10 <sup>7</sup>	±	1.42×10 <sup>6</sup>	3.62×10 <sup>7</sup>	±	6.82×10 <sup>6</sup>	9.19×10 <sup>5</sup>	±	8.03×10 <sup>4</sup>
											1.13×10 <sup>6</sup>	±	2.38×10 <sup>5</sup>
											1.55×10 <sup>6</sup>	±	2.26×10 <sup>5</sup>

**Table S5:** *nirK* and *nirS* gene abundances in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

Treatment	Depth (cm)	<i>nirK</i>						<i>nirS</i>					
		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point	
SRF	0-1	3.97×10 <sup>8</sup>	± 2.35×10 <sup>7</sup>	2.75×10 <sup>8</sup>	± 3.31×10 <sup>7</sup>	6.12×10 <sup>8</sup>	± 6.36×10 <sup>7</sup>	4.34×10 <sup>7</sup>	± 2.01×10 <sup>6</sup>	3.17×10 <sup>7</sup>	± 2.10×10 <sup>6</sup>	5.40×10 <sup>7</sup>	± 4.61×10 <sup>6</sup>
INC		3.73×10 <sup>8</sup>	± 9.67×10 <sup>6</sup>	2.99×10 <sup>8</sup>	± 3.35×10 <sup>7</sup>	5.54×10 <sup>8</sup>	± 7.72×10 <sup>7</sup>	4.58×10 <sup>7</sup>	± 3.45×10 <sup>6</sup>	3.45×10 <sup>7</sup>	± 3.47×10 <sup>6</sup>	4.35×10 <sup>7</sup>	± 3.00×10 <sup>6</sup>
CON		3.24×10 <sup>8</sup>	± 1.40×10 <sup>7</sup>	2.17×10 <sup>8</sup>	± 2.64×10 <sup>7</sup>	3.87×10 <sup>8</sup>	± 2.94×10 <sup>7</sup>	3.58×10 <sup>7</sup>	± 1.93×10 <sup>6</sup>	2.33×10 <sup>7</sup>	± 2.91×10 <sup>6</sup>	3.55×10 <sup>7</sup>	± 6.79×10 <sup>6</sup>
SRF+S		2.72×10 <sup>8</sup>	± 3.61×10 <sup>7</sup>	4.33×10 <sup>8</sup>	± 3.69×10 <sup>7</sup>	6.16×10 <sup>8</sup>	± 1.32×10 <sup>8</sup>	5.86×10 <sup>7</sup>	± 9.09×10 <sup>6</sup>	6.69×10 <sup>7</sup>	± 9.85×10 <sup>6</sup>	8.52×10 <sup>7</sup>	± 7.21×10 <sup>6</sup>
INS+S		2.81×10 <sup>8</sup>	± 6.73×10 <sup>7</sup>	5.67×10 <sup>8</sup>	± 5.81×10 <sup>7</sup>	5.46×10 <sup>8</sup>	± 2.86×10 <sup>7</sup>	7.32×10 <sup>7</sup>	± 1.43×10 <sup>7</sup>	9.65×10 <sup>7</sup>	± 1.69×10 <sup>7</sup>	8.99×10 <sup>7</sup>	± 7.18×10 <sup>6</sup>
CON+S		3.62×10 <sup>8</sup>	± 5.50×10 <sup>7</sup>	5.75×10 <sup>8</sup>	± 4.33×10 <sup>7</sup>	7.50×10 <sup>8</sup>	± 9.78×10 <sup>7</sup>	1.01×10 <sup>8</sup>	± 7.78×10 <sup>6</sup>	1.67×10 <sup>8</sup>	± 1.54×10 <sup>7</sup>	1.26×10 <sup>8</sup>	± 1.44×10 <sup>7</sup>
SRF	1-10	3.91×10 <sup>8</sup>	± 3.75×10 <sup>7</sup>	3.44×10 <sup>8</sup>	± 6.80×10 <sup>7</sup>	5.46×10 <sup>8</sup>	± 5.75×10 <sup>7</sup>	3.64×10 <sup>7</sup>	± 2.12×10 <sup>6</sup>	3.67×10 <sup>7</sup>	± 6.07×10 <sup>6</sup>	4.16×10 <sup>7</sup>	± 4.55×10 <sup>6</sup>
INC		3.55×10 <sup>8</sup>	± 2.92×10 <sup>7</sup>	3.32×10 <sup>8</sup>	± 4.49×10 <sup>7</sup>	5.72×10 <sup>8</sup>	± 9.32×10 <sup>7</sup>	4.52×10 <sup>7</sup>	± 3.15×10 <sup>6</sup>	3.25×10 <sup>7</sup>	± 5.19×10 <sup>6</sup>	5.19×10 <sup>7</sup>	± 3.54×10 <sup>6</sup>
CON		2.79×10 <sup>8</sup>	± 2.60×10 <sup>7</sup>	2.09×10 <sup>8</sup>	± 1.27×10 <sup>7</sup>	4.27×10 <sup>8</sup>	± 4.77×10 <sup>7</sup>	3.27×10 <sup>7</sup>	± 2.88×10 <sup>6</sup>	2.12×10 <sup>7</sup>	± 1.35×10 <sup>6</sup>	3.53×10 <sup>7</sup>	± 1.78×10 <sup>6</sup>
SRF+S		3.33×10 <sup>8</sup>	± 1.82×10 <sup>7</sup>	3.21×10 <sup>8</sup>	± 2.59×10 <sup>7</sup>	4.11×10 <sup>8</sup>	± 6.95×10 <sup>7</sup>	3.09×10 <sup>7</sup>	± 1.48×10 <sup>6</sup>	3.52×10 <sup>7</sup>	± 2.27×10 <sup>6</sup>	5.77×10 <sup>7</sup>	± 8.64×10 <sup>6</sup>
INS+S		4.19×10 <sup>8</sup>	± 3.41×10 <sup>7</sup>	4.25×10 <sup>8</sup>	± 2.81×10 <sup>7</sup>	5.70×10 <sup>8</sup>	± 8.24×10 <sup>7</sup>	4.58×10 <sup>7</sup>	± 5.62×10 <sup>6</sup>	4.48×10 <sup>7</sup>	± 3.07×10 <sup>6</sup>	7.99×10 <sup>7</sup>	± 4.90×10 <sup>6</sup>
CON+S		3.46×10 <sup>8</sup>	± 2.08×10 <sup>7</sup>	3.71×10 <sup>8</sup>	± 4.73×10 <sup>7</sup>	6.28×10 <sup>8</sup>	± 8.51×10 <sup>7</sup>	3.15×10 <sup>7</sup>	± 2.13×10 <sup>6</sup>	4.12×10 <sup>7</sup>	± 5.75×10 <sup>6</sup>	6.27×10 <sup>7</sup>	± 6.18×10 <sup>6</sup>
SRF	10-20	3.07×10 <sup>8</sup>	± 1.48×10 <sup>7</sup>	2.76×10 <sup>8</sup>	± 1.05×10 <sup>7</sup>	4.60×10 <sup>8</sup>	± 5.42×10 <sup>7</sup>	3.29×10 <sup>7</sup>	± 2.30×10 <sup>6</sup>	3.17×10 <sup>7</sup>	± 2.99×10 <sup>6</sup>	4.65×10 <sup>7</sup>	± 2.59×10 <sup>6</sup>
INC		3.08×10 <sup>8</sup>	± 4.24×10 <sup>7</sup>	2.31×10 <sup>8</sup>	± 1.67×10 <sup>7</sup>	6.25×10 <sup>8</sup>	± 1.80×10 <sup>8</sup>	3.82×10 <sup>7</sup>	± 5.28×10 <sup>6</sup>	2.03×10 <sup>7</sup>	± 1.46×10 <sup>6</sup>	5.21×10 <sup>7</sup>	± 9.97×10 <sup>6</sup>
CON		3.49×10 <sup>8</sup>	± 2.64×10 <sup>7</sup>	1.78×10 <sup>8</sup>	± 8.78×10 <sup>6</sup>	4.04×10 <sup>8</sup>	± 7.95×10 <sup>7</sup>	3.77×10 <sup>7</sup>	± 2.31×10 <sup>6</sup>	1.74×10 <sup>7</sup>	± 1.61×10 <sup>6</sup>	3.58×10 <sup>7</sup>	± 4.86×10 <sup>6</sup>
SRF+S		2.67×10 <sup>8</sup>	± 1.99×10 <sup>7</sup>	2.81×10 <sup>8</sup>	± 2.11×10 <sup>7</sup>	3.84×10 <sup>8</sup>	± 5.56×10 <sup>7</sup>	2.75×10 <sup>7</sup>	± 5.87×10 <sup>5</sup>	3.13×10 <sup>7</sup>	± 2.22×10 <sup>6</sup>	5.24×10 <sup>7</sup>	± 5.11×10 <sup>6</sup>
INS+S		3.70×10 <sup>8</sup>	± 4.49×10 <sup>7</sup>	4.25×10 <sup>8</sup>	± 5.32×10 <sup>7</sup>	5.20×10 <sup>8</sup>	± 6.65×10 <sup>7</sup>	3.72×10 <sup>7</sup>	± 4.45×10 <sup>6</sup>	4.35×10 <sup>7</sup>	± 5.69×10 <sup>6</sup>	6.96×10 <sup>7</sup>	± 3.55×10 <sup>6</sup>
CON+S		3.19×10 <sup>8</sup>	± 1.89×10 <sup>7</sup>	3.77×10 <sup>8</sup>	± 1.50×10 <sup>7</sup>	5.80×10 <sup>8</sup>	± 1.00×10 <sup>8</sup>	3.57×10 <sup>7</sup>	± 1.86×10 <sup>6</sup>	3.86×10 <sup>7</sup>	± 3.69×10 <sup>6</sup>	5.57×10 <sup>7</sup>	± 7.67×10 <sup>6</sup>

**Table S6:** *nosZI* and *nosZII* gene abundances in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

Treatment	Depth (cm)	<i>nosZI</i>						<i>nosZII</i>					
		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point	
SRF	0-1	2.19×10 <sup>8</sup>	± 5.44×10 <sup>6</sup>	1.32×10 <sup>8</sup>	± 9.66×10 <sup>6</sup>	3.02×10 <sup>8</sup>	± 2.50×10 <sup>7</sup>	2.13×10 <sup>7</sup>	± 2.50×10 <sup>6</sup>	1.48×10 <sup>7</sup>	± 9.21×10 <sup>5</sup>	3.06×10 <sup>7</sup>	± 2.71×10 <sup>6</sup>
INC		2.43×10 <sup>8</sup>	± 2.10×10 <sup>7</sup>	1.53×10 <sup>8</sup>	± 2.51×10 <sup>7</sup>	2.89×10 <sup>8</sup>	± 3.34×10 <sup>7</sup>	1.64×10 <sup>7</sup>	± 1.02×10 <sup>6</sup>	1.25×10 <sup>7</sup>	± 9.24×10 <sup>5</sup>	1.88×10 <sup>7</sup>	± 2.07×10 <sup>6</sup>
CON		1.88×10 <sup>8</sup>	± 1.69×10 <sup>7</sup>	9.84×10 <sup>7</sup>	± 1.64×10 <sup>7</sup>	1.89×10 <sup>8</sup>	± 3.04×10 <sup>7</sup>	1.85×10 <sup>7</sup>	± 2.21×10 <sup>6</sup>	1.04×10 <sup>7</sup>	± 1.36×10 <sup>6</sup>	1.73×10 <sup>7</sup>	± 3.06×10 <sup>6</sup>
SRF+S		2.16×10 <sup>8</sup>	± 2.88×10 <sup>7</sup>	2.78×10 <sup>8</sup>	± 3.33×10 <sup>7</sup>	3.57×10 <sup>8</sup>	± 6.22×10 <sup>7</sup>	1.97×10 <sup>7</sup>	± 3.27×10 <sup>6</sup>	3.12×10 <sup>7</sup>	± 3.51×10 <sup>6</sup>	3.49×10 <sup>7</sup>	± 4.47×10 <sup>6</sup>
INS+S		2.78×10 <sup>8</sup>	± 5.13×10 <sup>7</sup>	4.46×10 <sup>8</sup>	± 7.98×10 <sup>7</sup>	4.13×10 <sup>8</sup>	± 2.44×10 <sup>7</sup>	2.78×10 <sup>7</sup>	± 3.74×10 <sup>6</sup>	4.22×10 <sup>7</sup>	± 7.00×10 <sup>6</sup>	3.62×10 <sup>7</sup>	± 4.17×10 <sup>6</sup>
CON+S		3.91×10 <sup>8</sup>	± 3.95×10 <sup>7</sup>	5.89×10 <sup>8</sup>	± 4.34×10 <sup>7</sup>	5.19×10 <sup>8</sup>	± 5.03×10 <sup>7</sup>	2.97×10 <sup>7</sup>	± 3.21×10 <sup>6</sup>	4.59×10 <sup>7</sup>	± 5.11×10 <sup>6</sup>	4.53×10 <sup>7</sup>	± 3.00×10 <sup>6</sup>
SRF	1-10	1.87×10 <sup>8</sup>	± 1.46×10 <sup>7</sup>	1.64×10 <sup>8</sup>	± 3.70×10 <sup>7</sup>	2.38×10 <sup>8</sup>	± 2.64×10 <sup>7</sup>	1.46×10 <sup>7</sup>	± 8.89×10 <sup>5</sup>	1.68×10 <sup>7</sup>	± 2.67×10 <sup>6</sup>	2.01×10 <sup>7</sup>	± 1.73×10 <sup>6</sup>
INC		2.33×10 <sup>8</sup>	± 2.48×10 <sup>7</sup>	1.65×10 <sup>8</sup>	± 3.54×10 <sup>7</sup>	2.84×10 <sup>8</sup>	± 2.99×10 <sup>7</sup>	1.64×10 <sup>7</sup>	± 8.69×10 <sup>5</sup>	1.43×10 <sup>7</sup>	± 2.87×10 <sup>6</sup>	2.54×10 <sup>7</sup>	± 1.02×10 <sup>6</sup>
CON		1.51×10 <sup>8</sup>	± 1.60×10 <sup>7</sup>	8.79×10 <sup>7</sup>	± 9.85×10 <sup>6</sup>	1.95×10 <sup>8</sup>	± 2.22×10 <sup>7</sup>	1.42×10 <sup>7</sup>	± 1.04×10 <sup>6</sup>	9.64×10 <sup>6</sup>	± 7.71×10 <sup>5</sup>	1.99×10 <sup>7</sup>	± 1.86×10 <sup>6</sup>
SRF+S		1.48×10 <sup>8</sup>	± 1.28×10 <sup>7</sup>	1.52×10 <sup>8</sup>	± 1.31×10 <sup>7</sup>	2.15×10 <sup>8</sup>	± 4.58×10 <sup>7</sup>	1.03×10 <sup>7</sup>	± 3.35×10 <sup>5</sup>	1.36×10 <sup>7</sup>	± 7.67×10 <sup>5</sup>	1.75×10 <sup>7</sup>	± 2.97×10 <sup>6</sup>
INS+S		2.33×10 <sup>8</sup>	± 3.55×10 <sup>7</sup>	2.40×10 <sup>8</sup>	± 2.07×10 <sup>7</sup>	3.25×10 <sup>8</sup>	± 2.94×10 <sup>7</sup>	1.87×10 <sup>7</sup>	± 2.39×10 <sup>6</sup>	2.85×10 <sup>7</sup>	± 1.36×10 <sup>6</sup>	3.47×10 <sup>7</sup>	± 2.55×10 <sup>6</sup>
CON+S		1.65×10 <sup>8</sup>	± 7.22×10 <sup>6</sup>	1.90×10 <sup>8</sup>	± 3.00×10 <sup>7</sup>	3.26×10 <sup>8</sup>	± 4.30×10 <sup>7</sup>	1.13×10 <sup>7</sup>	± 1.29×10 <sup>6</sup>	1.91×10 <sup>7</sup>	± 2.55×10 <sup>6</sup>	2.70×10 <sup>7</sup>	± 2.43×10 <sup>6</sup>
SRF	10-20	1.62×10 <sup>8</sup>	± 1.29×10 <sup>7</sup>	1.34×10 <sup>8</sup>	± 1.56×10 <sup>7</sup>	2.26×10 <sup>8</sup>	± 2.55×10 <sup>7</sup>	1.11×10 <sup>7</sup>	± 1.11×10 <sup>6</sup>	1.16×10 <sup>7</sup>	± 1.70×10 <sup>6</sup>	1.73×10 <sup>7</sup>	± 8.82×10 <sup>5</sup>
INC		1.89×10 <sup>8</sup>	± 3.69×10 <sup>7</sup>	8.32×10 <sup>7</sup>	± 1.04×10 <sup>7</sup>	2.84×10 <sup>8</sup>	± 8.16×10 <sup>7</sup>	1.15×10 <sup>7</sup>	± 1.87×10 <sup>6</sup>	7.30×10 <sup>6</sup>	± 6.03×10 <sup>5</sup>	2.62×10 <sup>7</sup>	± 5.75×10 <sup>6</sup>
CON		1.37×10 <sup>8</sup>	± 3.18×10 <sup>7</sup>	7.04×10 <sup>7</sup>	± 7.32×10 <sup>6</sup>	1.65×10 <sup>8</sup>	± 3.14×10 <sup>7</sup>	1.41×10 <sup>7</sup>	± 6.20×10 <sup>5</sup>	7.64×10 <sup>6</sup>	± 7.11×10 <sup>5</sup>	1.63×10 <sup>7</sup>	± 2.35×10 <sup>6</sup>
SRF+S		1.14×10 <sup>8</sup>	± 7.00×10 <sup>6</sup>	1.22×10 <sup>8</sup>	± 1.10×10 <sup>7</sup>	1.79×10 <sup>8</sup>	± 2.65×10 <sup>7</sup>	7.95×10 <sup>6</sup>	± 1.62×10 <sup>5</sup>	1.05×10 <sup>7</sup>	± 1.61×10 <sup>6</sup>	1.45×10 <sup>7</sup>	± 1.45×10 <sup>6</sup>
INS+S		1.60×10 <sup>8</sup>	± 2.00×10 <sup>7</sup>	1.85×10 <sup>8</sup>	± 2.85×10 <sup>7</sup>	2.49×10 <sup>8</sup>	± 1.89×10 <sup>7</sup>	1.13×10 <sup>7</sup>	± 1.63×10 <sup>6</sup>	1.92×10 <sup>7</sup>	± 2.01×10 <sup>6</sup>	2.17×10 <sup>7</sup>	± 4.78×10 <sup>5</sup>
CON+S		1.77×10 <sup>8</sup>	± 1.44×10 <sup>7</sup>	1.84×10 <sup>8</sup>	± 2.26×10 <sup>7</sup>	2.45×10 <sup>8</sup>	± 3.90×10 <sup>7</sup>	1.19×10 <sup>7</sup>	± 1.13×10 <sup>6</sup>	1.67×10 <sup>7</sup>	± 2.76×10 <sup>6</sup>	2.27×10 <sup>7</sup>	± 3.49×10 <sup>6</sup>

**Table S7:** *amoA* AOA/AOB, *nirK/nirS* and *nosZI/nosZII* gene abundance ratios in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

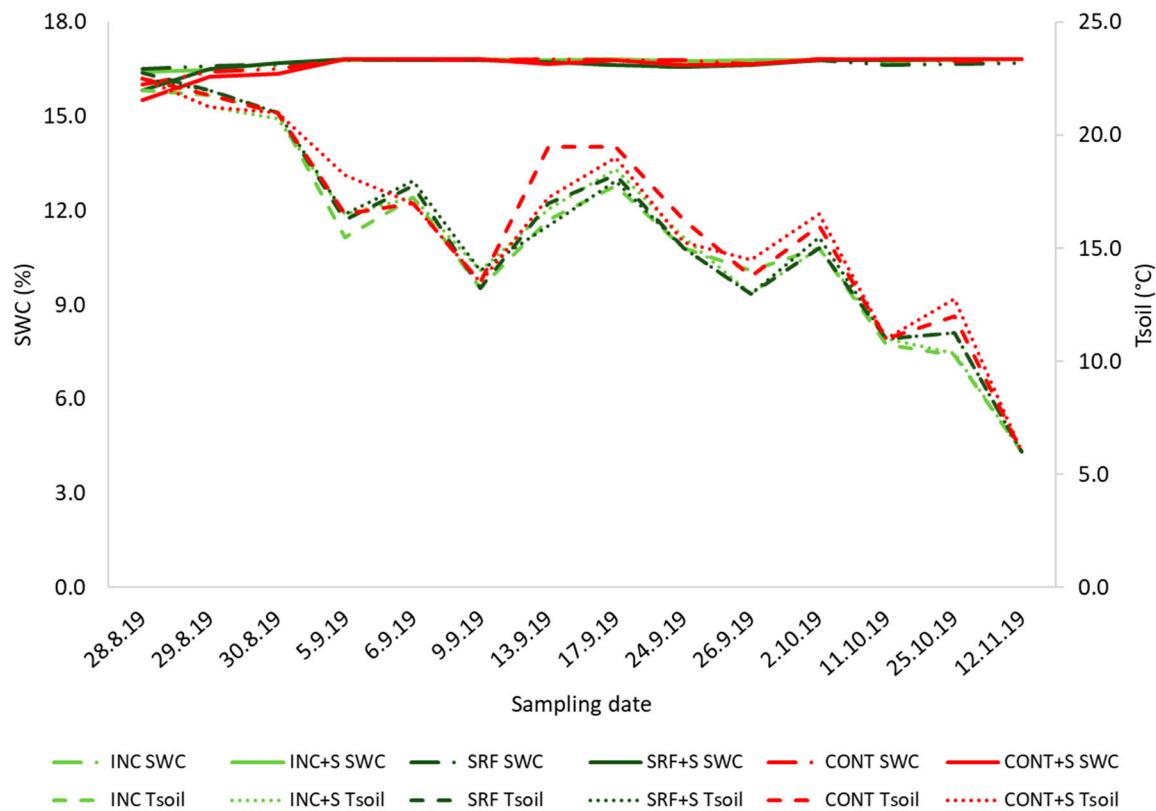
Treatment	Depth (cm)	AOA/AOB			<i>nirK/nirS</i>			<i>nosZI/nosZII</i>		
		1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point	1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point	1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point
SRF	<b>0-1</b>	11.1 ± 0.8	11.0 ± 2.3	7.5 ± 0.9	9.2 ± 0.7	8.6 ± 0.5	11.7 ± 1.7	10.6 ± 1.1	9.0 ± 0.8	9.9 ± 0.6
INC		12.0 ± 0.5	11.5 ± 0.5	9.7 ± 1.4	8.2 ± 0.5	8.8 ± 0.7	12.7 ± 1.2	14.9 ± 1.6	12.2 ± 1.8	17.0 ± 2.6
CON		9.1 ± 0.7	10.3 ± 0.1	12.1 ± 0.5	9.1 ± 0.5	9.4 ± 0.6	11.9 ± 1.9	10.3 ± 0.4	9.6 ± 1.5	11.4 ± 1.3
SRF+S		4.7 ± 0.9	1.3 ± 0.2	2.5 ± 0.6	4.7 ± 0.1	6.6 ± 0.4	7.0 ± 1.2	11.2 ± 1.2	8.9 ± 0.3	10.0 ± 0.8
INS+S		4.0 ± 0.4	2.3 ± 0.2	2.0 ± 0.4	3.7 ± 0.3	6.2 ± 0.7	6.2 ± 0.7	9.8 ± 0.8	10.5 ± 0.4	11.8 ± 1.2
CON+S		4.8 ± 0.3	2.1 ± 0.9	0.8 ± 0.1	3.6 ± 0.5	3.5 ± 0.4	5.9 ± 0.2	13.2 ± 0.4	13.2 ± 1.3	11.4 ± 0.5
SRF	<b>1-10</b>	15.5 ± 0.9	16.3 ± 0.8	19.0 ± 1.1	10.7 ± 0.6	9.2 ± 0.3	13.4 ± 1.5	12.8 ± 0.6	9.7 ± 0.9	11.8 ± 0.5
INC		13.3 ± 1.0	11.1 ± 1.3	12.8 ± 1.3	7.9 ± 0.4	10.5 ± 0.9	11.0 ± 1.6	14.1 ± 0.9	11.6 ± 0.9	11.1 ± 0.8
CON		12.2 ± 0.8	18.3 ± 1.5	19.6 ± 2.2	8.6 ± 0.6	9.9 ± 0.4	12.0 ± 1.1	10.6 ± 0.6	9.1 ± 0.4	9.8 ± 0.7
SRF+S		10.5 ± 0.5	7.4 ± 1.8	11.4 ± 2.2	10.8 ± 0.7	9.1 ± 0.4	7.1 ± 0.6	14.3 ± 1.1	11.3 ± 1.2	11.8 ± 0.9
INS+S		7.7 ± 1.0	8.0 ± 1.6	8.3 ± 1.5	9.3 ± 0.6	9.5 ± 0.5	7.2 ± 1.1	12.5 ± 1.2	8.4 ± 0.7	9.4 ± 0.7
CON+S		12.9 ± 0.9	9.6 ± 1.5	8.2 ± 1.1	11.0 ± 0.2	9.0 ± 0.3	9.9 ± 0.5	15.0 ± 1.3	9.8 ± 0.4	12.0 ± 0.8
SRF	<b>10-20</b>	16.3 ± 1.2	21.7 ± 0.9	20.0 ± 1.6	9.4 ± 0.4	9.0 ± 1.0	9.8 ± 0.8	14.7 ± 0.5	11.7 ± 0.4	12.9 ± 1.0
INC		15.5 ± 1.3	14.2 ± 1.4	15.7 ± 2.5	8.1 ± 0.2	11.4 ± 0.6	11.5 ± 1.1	16.1 ± 0.8	11.3 ± 0.9	10.4 ± 0.9
CON		14.8 ± 0.4	19.2 ± 2.1	25.4 ± 1.8	9.3 ± 0.4	10.4 ± 0.6	11.1 ± 0.9	9.9 ± 2.4	9.3 ± 0.7	10.2 ± 1.3
SRF+S		15.6 ± 1.4	20.0 ± 2.3	27.2 ± 3.2	9.6 ± 0.5	9.1 ± 0.9	7.3 ± 1.0	14.3 ± 0.6	12.0 ± 0.8	12.1 ± 0.8
INS+S		11.4 ± 0.7	14.5 ± 1.8	21.9 ± 2.3	10.1 ± 1.0	9.8 ± 0.4	7.6 ± 1.3	14.4 ± 0.7	9.6 ± 0.1	11.5 ± 0.8
CON+S		15.0 ± 1.2	17.8 ± 2.5	23.1 ± 2.7	8.9 ± 0.4	9.9 ± 0.6	10.3 ± 0.5	14.9 ± 0.5	11.2 ± 0.6	10.8 ± 0.7

**Table S8:** ITS/16S rRNA bacteria, *nirK*/16S rRNA bacteria and *nirS*/16S rRNA bacteria gene abundance ratios in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

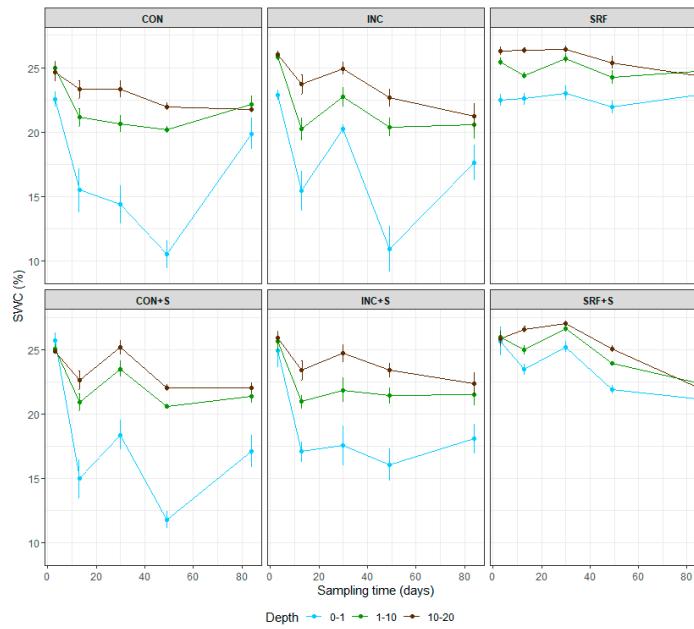
Treatment	Depth (cm)	ITS/16S rRNA bact.						<i>nirK</i> /16S rRNA bact.						<i>nirS</i> /16S rRNA bact.					
		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point		1 <sup>st</sup> sampling point		2 <sup>nd</sup> sampling point		4 <sup>th</sup> sampling point	
SRF	0-1	0.09	± 0.009	0.08	± 0.010	0.13	± 0.014	0.22	± 0.7	0.17	± 0.6	0.25	± 1.7	0.02	± 0.002	0.02	± 0.001	0.02	± 0.001
INC		0.09	± 0.009	0.08	± 0.007	0.07	± 0.032	0.21	± 0.5	0.19	± 0.7	0.22	± 1.2	0.03	± 0.001	0.02	± 0.002	0.02	± 0.001
CON		0.05	± 0.005	0.04	± 0.003	0.08	± 0.014	0.18	± 0.5	0.18	± 0.6	0.20	± 1.9	0.02	± 0.001	0.02	± 0.001	0.02	± 0.001
SRF+S		0.07	± 0.010	0.07	± 0.001	0.10	± 0.016	0.09	± 0.1	0.16	± 0.4	0.17	± 1.2	0.02	± 0.002	0.02	± 0.002	0.02	± 0.000
INS+S		0.07	± 0.014	0.10	± 0.007	0.05	± 0.003	0.07	± 0.3	0.14	± 0.7	0.14	± 0.7	0.02	± 0.002	0.02	± 0.002	0.02	± 0.001
CON+S		0.02	± 0.003	0.03	± 0.003	0.07	± 0.005	0.08	± 0.5	0.09	± 0.4	0.15	± 0.2	0.02	± 0.002	0.02	± 0.001	0.03	± 0.001
SRF	1-10	0.06	± 0.010	0.04	± 0.004	0.06	± 0.003	0.26	± 0.6	0.20	± 0.3	0.27	± 1.5	0.02	± 0.001	0.02	± 0.002	0.02	± 0.002
INC		0.08	± 0.004	0.10	± 0.007	0.10	± 0.009	0.19	± 0.4	0.22	± 0.9	0.24	± 1.6	0.02	± 0.001	0.02	± 0.002	0.02	± 0.001
CON		0.04	± 0.002	0.04	± 0.003	0.05	± 0.007	0.18	± 0.6	0.20	± 0.4	0.22	± 1.1	0.02	± 0.001	0.02	± 0.001	0.02	± 0.001
SRF+S		0.05	± 0.005	0.04	± 0.006	0.04	± 0.005	0.20	± 0.7	0.18	± 0.4	0.17	± 0.6	0.02	± 0.001	0.02	± 0.000	0.02	± 0.002
INS+S		0.11	± 0.011	0.09	± 0.009	0.11	± 0.018	0.22	± 0.6	0.16	± 0.5	0.18	± 1.1	0.02	± 0.001	0.02	± 0.001	0.02	± 0.000
CON+S		0.04	± 0.002	0.04	± 0.005	0.05	± 0.003	0.25	± 0.2	0.17	± 0.3	0.23	± 0.5	0.02	± 0.001	0.02	± 0.001	0.02	± 0.001
SRF	10-20	0.04	± 0.001	0.05	± 0.006	0.07	± 0.021	0.23	± 0.4	0.20	± 1.0	0.24	± 0.8	0.02	± 0.001	0.02	± 0.002	0.02	± 0.001
INC		0.05	± 0.002	0.05	± 0.004	0.06	± 0.006	0.21	± 0.2	0.25	± 0.6	0.28	± 1.1	0.03	± 0.002	0.02	± 0.000	0.02	± 0.002
CON		0.04	± 0.003	0.04	± 0.005	0.07	± 0.019	0.22	± 0.4	0.20	± 0.6	0.23	± 0.9	0.02	± 0.002	0.02	± 0.001	0.02	± 0.001
SRF+S		0.04	± 0.002	0.04	± 0.005	0.04	± 0.006	0.23	± 0.5	0.18	± 0.9	0.19	± 1.0	0.02	± 0.001	0.02	± 0.001	0.03	± 0.001
INS+S		0.05	± 0.006	0.08	± 0.027	0.04	± 0.006	0.25	± 1.0	0.21	± 0.4	0.21	± 1.3	0.02	± 0.001	0.02	± 0.001	0.03	± 0.001
CON+S		0.05	± 0.004	0.05	± 0.013	0.07	± 0.020	0.23	± 0.4	0.20	± 0.6	0.24	± 0.5	0.03	± 0.001	0.02	± 0.001	0.02	± 0.002

**Table S9:**  $(nosZI + nosZII)/16S$  rRNA bacteria and  $(nirK + nirS + nosZI + nosZII)/16S$  rRNA bacteria gene abundance ratios in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm) and three sampling points. Averages and standard errors of 4 replicates are shown

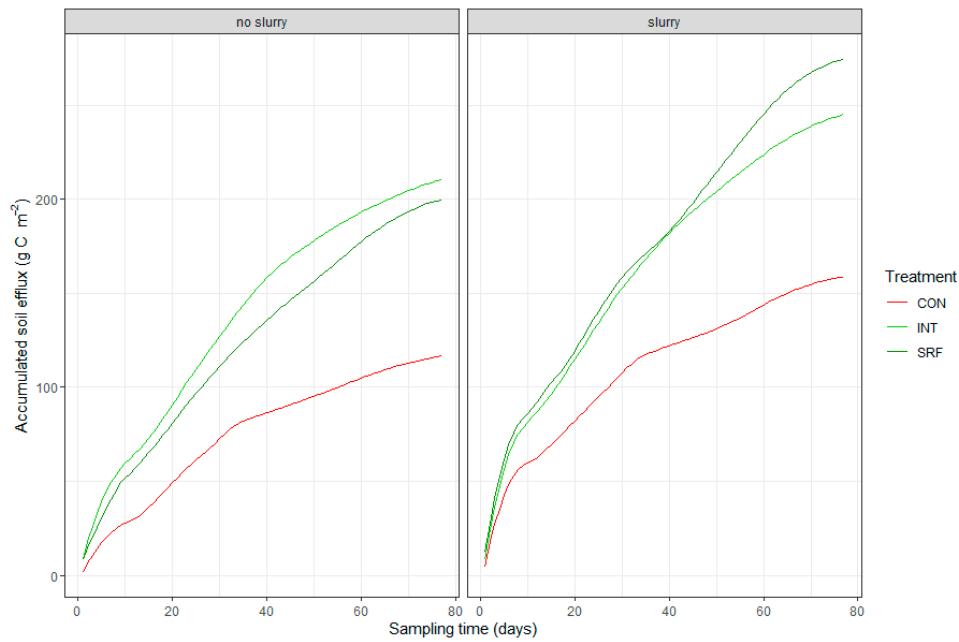
Treatment	Depth (cm)	$(nosZI + nosZII)/16S$ rRNA bact.			$(nirK + nirS + nosZI + nosZII)/16S$ rRNA bact.		
		1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point	1 <sup>st</sup> sampling point	2 <sup>nd</sup> sampling point	4 <sup>th</sup> sampling point
SRF	0-1	0.13 ± 0.01	0.09 ± 0.01	0.13 ± 0.01	0.38 ± 0.02	0.28 ± 0.03	0.40 ± 0.04
INC		0.15 ± 0.01	0.11 ± 0.01	0.10 ± 0.03	0.38 ± 0.02	0.32 ± 0.02	0.28 ± 0.10
CON		0.11 ± 0.00	0.09 ± 0.01	0.10 ± 0.01	0.32 ± 0.02	0.30 ± 0.02	0.32 ± 0.02
SRF+S		0.08 ± 0.01	0.11 ± 0.00	0.11 ± 0.01	0.18 ± 0.02	0.29 ± 0.01	0.30 ± 0.04
INS+S		0.08 ± 0.01	0.12 ± 0.01	0.12 ± 0.01	0.18 ± 0.02	0.28 ± 0.01	0.29 ± 0.01
CON+S		0.09 ± 0.01	0.09 ± 0.00	0.11 ± 0.00	0.19 ± 0.01	0.20 ± 0.02	0.29 ± 0.01
SRF	1-10	0.13 ± 0.01	0.11 ± 0.01	0.13 ± 0.01	0.41 ± 0.02	0.33 ± 0.03	0.42 ± 0.03
INC		0.14 ± 0.01	0.11 ± 0.02	0.13 ± 0.01	0.35 ± 0.03	0.36 ± 0.04	0.40 ± 0.05
CON		0.11 ± 0.01	0.09 ± 0.01	0.11 ± 0.01	0.31 ± 0.02	0.32 ± 0.02	0.35 ± 0.03
SRF+S		0.10 ± 0.01	0.09 ± 0.01	0.09 ± 0.02	0.32 ± 0.02	0.29 ± 0.02	0.29 ± 0.04
INS+S		0.13 ± 0.01	0.10 ± 0.01	0.11 ± 0.01	0.37 ± 0.01	0.28 ± 0.01	0.31 ± 0.03
CON+S		0.13 ± 0.01	0.10 ± 0.01	0.13 ± 0.01	0.41 ± 0.02	0.28 ± 0.01	0.38 ± 0.02
SRF	10-20	0.13 ± 0.01	0.10 ± 0.01	0.13 ± 0.01	0.39 ± 0.02	0.33 ± 0.04	0.40 ± 0.03
INC		0.13 ± 0.02	0.10 ± 0.01	0.14 ± 0.02	0.36 ± 0.03	0.36 ± 0.02	0.44 ± 0.07
CON		0.10 ± 0.02	0.09 ± 0.01	0.11 ± 0.01	0.34 ± 0.03	0.31 ± 0.01	0.36 ± 0.04
SRF+S		0.10 ± 0.01	0.08 ± 0.00	0.09 ± 0.01	0.35 ± 0.03	0.29 ± 0.02	0.30 ± 0.05
INS+S		0.11 ± 0.01	0.08 ± 0.03	0.11 ± 0.01	0.38 ± 0.03	0.34 ± 0.02	0.35 ± 0.04
CON+S		0.14 ± 0.01	0.10 ± 0.01	0.11 ± 0.01	0.40 ± 0.02	0.32 ± 0.01	0.38 ± 0.03



**Figure S1:** Measurements of soil water content (SWC) and soil temperature (T) at depth 10 cm in CON, INC and SRF soil treatments in presence/absence of slurry (S). Averages of 4 replicates are shown



**Figure S2:** Measurements of soil water content (SWC) in CON, INC and SRF soil treatments in presence/absence of slurry (S) at three sampling depths (cm). Averages and standard errors of 4 replicates are shown



**Figure S3:** Cumulative CO<sub>2</sub> effluxes (g C m<sup>-2</sup>) in CON, INC and SRF soil treatments in presence/absence of slurry (S). Averages of 4 replicates are shown